

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Schmidt, Eduard Daniel Leendert
De Vries, Sape Cornelis
Hecht, Valerie France Gabrielle
- (ii) TITLE OF INVENTION: Apomixis Conferred By Expression of SERK
Interacting Proteins
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Syngenta Patent Dept.
 - (B) STREET: 3054 Cornwallis Road
 - (C) CITY: RTP
 - (D) STATE: NC
 - (E) COUNTRY: USA
 - (F) ZIP: 27709
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/EP99/07972
 - (B) FILING DATE: 20-OCT-1999
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Meigs, J. Timothy
 - (B) REGISTRATION NUMBER: 38,241
 - (C) REFERENCE/DOCKET NUMBER: S-30683A
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 919-541-8587

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 551 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: 3A35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACGTGTCGGT GGAGCGGGT CGGGTCAGTC GGGTCAGATA CCAAGGTGCC AAGTGAAGG	60
TTGTGGGATG GATCTAACCA ATGCAAAAGG TTATTACTCG AGACACCGAG TTTGTGGAGT	120
GCACTCTAAA ACACCTAAAG TCACTGTGGC TGGTATCGAA CAGAGGTTTT GTCAACAGTG	180
CAGCAGGTTT CATCAGCTTC CGGAATTTGA CCTAGAGAAA AGGAGTTGCC GCAGGAGACT	240
CGCTGGTCAT AATGAGCGAC GAAGGAAGCC ACAGCCTGCG TCTCTCTCTG TGTTAGCTTC	300
TCGTTACGGG AGGATCGCAC CTTCGCTTTA CGAAAATGGT GATGCTGGAA TGAATGGAAG	360
CTTTCTTGGG AACCAAGAGA TAGGATGGCC AAGTTCAAGA ACATTGGATA CAAGAGTGAT	420
GAGGCGGCCA GTGTCATCAC CGTCATGGCA GATCAATCCA ATGAATGTAT TTAGTCAAGG	480
TTCAGTTGGT GGAGGAAGGA CAAGCTTCTC ATCTCCAGAG ATTATGGACA CTAAACTAGA	540
GAGCTACAAG G	551

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: 3A35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Glu	Met	Gly	Ser	Asn	Ser	Gly	Pro	Gly	His	Gly	Pro	Gly	Gln	Ala	1	5	10	15
Glu	Ser	Gly	Gly	Ser	Ser	Thr	Glu	Ser	Ser	Ser	Phe	Ser	Gly	Gly	Leu	20	25	30	
Met	Phe	Gly	Gln	Lys	Ile	Tyr	Phe	Glu	Asp	Gly	Gly	Gly	Gly	Ser	Gly	35	40	45	
Ser	Ser	Ser	Ser	Gly	Gly	Arg	Ser	Asn	Arg	Arg	Val	Arg	Gly	Gly	Gly	50	55	60	
Ser	Gly	Gln	Ser	Gly	Gln	Ile	Pro	Arg	Cys	Gln	Val	Glu	Gly	Cys	Gly	65	70	75	80
Met	Asp	Leu	Thr	Asn	Ala	Lys	Gly	Tyr	Tyr	Ser	Arg	His	Arg	Val	Cys	85	90	95	
Gly	Val	His	Ser	Lys	Thr	Pro	Lys	Val	Thr	Val	Ala	Gly	Ile	Glu	Gln	100	105	110	
Arg	Phe	Cys	Gln	Gln	Cys	Ser	Arg	Phe	His	Gln	Leu	Pro	Glu	Phe	Asp	115	120	125	
Leu	Glu	Lys	Arg	Ser	Cys	Arg	Arg	Arg	Leu	Ala	Gly	His	Asn	Glu	Arg	130	135	140	
Arg	Arg	Lys	Pro	Gln	Pro	Ala	Ser	Leu	Ser	Val	Leu	Ala	Ser	Arg	Tyr	145	150	155	160
Gly	Arg	Ile	Ala	Pro	Ser	Leu	Tyr	Glu	Asn	Gly	Asp	Ala	Gly	Met	Asn	165	170	175	
Gly	Ser	Phe	Leu	Gly	Asn	Gln	Glu	Ile	Gly	Trp	Pro	Ser	Ser	Arg	Thr	180	185	190	
Leu	Asp	Thr	Arg	Val	Met	Arg	Arg	Pro	Val	Ser	Ser	Pro	Ser	Trp	Gln	195	200	205	
Ile	Asn	Pro	Met	Asn	Val	Phe	Ser	Gln	Gly	Ser	Val	Gly	Gly	Gly	Arg	210	215	220	
Thr	Ser	Phe	Ser	Ser	Pro	Glu	Ile	Met	Asp	Thr	Lys	Leu	Glu	Ser	Tyr				

225		230		235		240
Lys Gly Ile Gly Asp Ser Asn Cys Ala Leu Ser Leu Leu Ser Asn Pro						
	245		250		255	
His Gln Pro His Asp Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn						
	260		265		270	
Asn Asn Asn Thr Trp Arg Ala Ser Ser Gly Phe Gly Pro Met Thr Val						
	275		280		285	
Thr Met Ala Gln Pro Pro Pro Ala Pro Ser Gln His Gln Tyr Leu Asn						
	290		295		300	
Pro Pro Trp Val Phe Lys Asp Asn Asp Asn Asp Met Ser Pro Val Leu						
	305		310		315	
Asn Leu Gly Arg Tyr Thr Glu Pro Asp Asn Cys Gln Ile Ser Ser Gly						
	325		330		335	
Thr Ala Met Gly Glu Phe Glu Leu Ser Asp His His His Gln Ser Arg						
	340		345		350	
Arg Gln Tyr Met Glu Asp Glu Asn Thr Arg Ala Tyr Asp Ser Ser Ser						
	355		360		365	
His His Thr Asn Trp Ser Leu						
	370		375			

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 859 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 3B39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCAACATGTC TTCCTAACCA GAAATCCACC ATCATCTTCC CACGAATACA ACTTAAAGCT	60
TTACCAGAAA ATGGAGGGTC AGAGAACACA ACGCCGGGGT TACTTGAAAG ACAAGGCTAC	120
AGTCTCCAAC CTTGTTGAAG AAGAAATGGA GAATGGCATG GATGGAGAAG AGGAGGATGG	180
AGGAGACGAA GACAAAAGGA AGAAGGTGAT GGAAAGAGTT AGAGGTCCTA GCACTGACCG	240
TGTTCCATCG CGACTGTGCC AGGTCGATAG GTGCACTGTT AATTTGACTG AGGCCAAGCA	300
GTATTACCGC AGACACAGAG TATGTGAAGT ACATGCAAAG GCATCTGCTG CGACTGTTGC	360
AGGGGTCAGG CAACGCTTTT GTCAACAATG CAGCAGGTTT CATGAGCTAC CAGAGTTTGA	420
TGAAGCTAAA AGAAGCTGCA GGAGGCGCTT AGCTGGACAC AATGAGAGGA GGAGGAAGAT	480
CTCTGGTGAC AGTTTTGGAG AAGGGTCAGG CCGGAGAGGG TTTAGCGGTC AACTGATCCA	540
GACTCAAGAA AGAAACAGGG TAGACAGGAA ACTTCCTATG ACCAACTCAT CATTTAAGGG	600
ACCACAGATC AGATAAACCC TCCCGCTCTC TCTCTTCTGT CATCTACATA TGCTCTATCT	660
ACACTCTTAT TAGACAAATA ATGGCATCTA ACAATGTCAA GAAAAGTTGG TCATGGTATT	720
AAATCCTAGA GGGAAATATA AGTATAAACC TTTAGTCCCC TTTATGCTGT CCTGTAATGA	780
ATATCTATCC GGAAATGTAT TCGCATAGTC TTGCGTCTAA TAATGTTTAT TAAAAAAAAA	840
AAAAAAAAAA AAAAAAAAAA	859

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: 3B39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Glu Gly Gln Arg Thr Gln Arg Arg Gly Tyr Leu Lys Asp Lys Ala
 1 5 10 15
 Thr Val Ser Asn Leu Val Glu Glu Glu Met Glu Asn Gly Met Asp Gly
 20 25 30
 Glu Glu Glu Asp Gly Gly Asp Glu Asp Lys Arg Lys Lys Val Met Glu
 35 40 45
 Arg Val Arg Gly Pro Ser Thr Asp Arg Val Pro Ser Arg Leu Cys Gln
 50 55 60
 Val Asp Arg Cys Thr Val Asn Leu Thr Glu Ala Lys Gln Tyr Tyr Arg
 65 70 75 80
 Arg His Arg Val Cys Glu Val His Ala Lys Ala Ser Ala Ala Thr Val
 85 90 95
 Ala Gly Val Arg Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Glu
 100 105 110
 Leu Pro Glu Phe Asp Glu Ala Lys Arg Ser Cys Arg Arg Arg Leu Ala
 115 120 125
 Gly His Asn Glu Arg Arg Arg Lys Ile Ser Gly Asp Ser Phe Gly Glu
 130 135 140
 Gly Ser Gly Arg Arg Gly Phe Ser Gly Gln Leu Ile Gln Thr Gln Glu
 145 150 155 160
 Arg Asn Arg Val Asp Arg Lys Leu Pro Met Thr Asn Ser Ser Phe Lys
 165 170 175
 Gly Pro Gln Ile Arg
 180

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: 4B19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AGAAGCAGAA AGGTAAAGCT ACAAGTAGTA GTGGAGTTTG TCAGGTCGAG AGTTGTACCG	60
CGGATATGAG CAAAGCCAAA CAGTACCACA AACGACACAA AGTCTGCCAG TTTCATGCCA	120
AAGCTCCTCA TGTTCCGATC TCTGGTCTTC ACCAACGTTT CTGCCAACAA TGCAGCAGGT	180
TTCACGCGCT CAGTGAGTTT GATGAAGCCA AGCGGAGTTG CAGGAGACGC TTAGCTGGAC	240
ACAACGAGAG AAGGCGGAAA AGCACAACCTG ACTAAAGACG GTGAAACGTG TGAGATCCCG	300
GTTTGAAGGT TAATGAAACA GGCTTTGCTT ACTCTCTTCT GTCAGTCTCT TTTAGCTCCT	360
TGTAATCCTC TGIGTCTCTG TCTGTTTCTC CATATTACCT GTAATCAAAG CTATCTGCTA	420
AACCTACGAC ATGGTTAAAT AAATGCATTG AGACTTAAAA AAAAAAAAAA AAAAAAAAAA	479

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: 4B19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ser Met Arg Arg Ser Lys Ala Glu Gly Lys Arg Ser Leu Arg Glu
1 5 10 15

Leu Ser Glu Glu Glu Glu Glu Glu Glu Glu Thr Glu Asp Glu Asp Thr
20 25 30

Phe Glu Glu Glu Glu Ala Leu Glu Lys Lys Gln Lys Gly Lys Ala Thr
35 40 45

Ser Ser Ser Gly Val Cys Gln Val Glu Ser Cys Thr Ala Asp Met Ser
50 55 60

Lys Ala Lys Gln Tyr His Lys Arg His Lys Val Cys Gln Phe His Ala
65 70 75 80

Lys Ala Pro His Val Arg Ile Ser Gly Leu His Gln Arg Phe Cys Gln
85 90 95

Gln Cys Ser Arg Phe His Ala Leu Ser Glu Phe Asp Glu Ala Lys Arg
100 105 110

Ser Cys Arg Arg Arg Leu Ala Gly His Asn Glu Arg Arg Arg Lys Ser
115 120 125

Thr Thr Asp
130

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: 3A52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCCATTCAAG GAGACACTAA TGGTGCTCTT ACTTTGAATC TTAATGGTGA AAGTGATGGC	60
CTTTTTCCTG CCAAGAAGAC CAAATCCGGA GCCGTTTGTC AGGTCGAAAA CTGTGAAGCT	120
GATCTTAGTA AAGTTAAGGA TTATCATAGA CGCCATAAGG TCTGTGAGAT GCATTCCAAG	180
GCTACTAGTG CCACTGTGGG AGGTATCTTG CAGCGCTTTT GTCAGCAATG TAGTAGGTTT	240
CATCTTCTGC CAGGTTTCGA TGACGGAAAG AGAAGTTGTC GTAGACGTTT GGCTGGCCAT	300
AATAAACGTC CGAGGAAAC AAATCCCGAA CCTGGCGCTA ACGGGAATCC TAGTGATGAT	360
CACTCAAGCA ACTATCTCTT GATTACTCTC TTGAAGATAC TCTCCAATAT GCATAACCAT	420
ACCGGTGATC AAGATTTGAT GTCTCATCTT CTGAAGAGCC TCGTAAGCCA TGCTGGCGAA	480
CAGTTAGGGA AAAACTTAGT TGAACCTCTT CTACAAGGAG AGATCTCAAG GTTCCTTAAA	540
ATATTGGAAA ACTCGGCTTT GCTTGGGATT GAGCAAGCTC CTCAAGAGGA GTTAAAGCAA	600
TTTTGGGCTC GGCAAGATGG GACAGCTACC GAGAACAGAT CAGAAAAACA AGTCAAAATG	660
AATGATTTTG ATTTGAATGA TATCTATATA GACTCAGATG ACACAGACGT CGAAAGATCT	720
CCTCCTCCAA CGAATCCAGC GACCAGTTCT CTTGATTATC CTTCATGGAT ACATCAGTCT	780
AGTCCGCCTC AGACAAGTAG GAATTCAGAT TCAGCATCTG ACCAGTCACC CTCAAGTTCT	840
AGTGAAGATG CTCAGATGCG CACAGGCCGG ATTGTGTTCA AACTATTTGG GAAAGAGCCA	900
AATGAATTTT CTATTGTCTT ACGAGGACAG ATTCTTGACT GGTATTCGCA TAGTCCAAC	960
GACATGGAGA GCTACATAAG ACCTGGCTGT ATCGTATTGA CCATCTATCT TCGTCAAGCT	1020
GAAACTGCTT GGAAGAACT TTCAGACGAT CTGGGTTTGA GCTTAGGGAA GCTTCTAGAT	1080
CTCTCCGATG ATCCCTTG TG GACAACCTGGA TGGATTATG TAGGGTGCAG AACCAACTTG	1140
CATTGTGATA TAACGGTCAG GTTGTGTTG ACACCTTCATT GTCTCTAAAA AGTCGTGATT	1200
ATAGTCACAT CATTAGCGTT AAACCGCTTG CTATAGCTGC AACGGAGAAG GCTCAATTTA	1260

CAGTTAAAGG	CATGAATCTC	CGTCGGCGTG	GCACAAGGTT	ACTTTGTTCT	GTTGAAGGAA	1320
AATACTTGAT	TCAGGAAACA	ACACACGATT	CGACGACCAG	GGAGGATGAC	GATTTCAAGG	1380
ACAACAGTGA	GATTGTTGAG	TGTGTAAACT	TCTCTTGTTG	TATGCCTATA	TTGAGTGGTC	1440
GAGGATTCAT	GGAGATTGAA	GACCAAGGAC	TCAGTAGCAG	CTTCTTCCCT	TTCTTAGTGG	1500
TTGAAGATGA	CGATGTTTGT	TCTGAAATCC	GTATACTTGA	AACCACATTA	GAGTTCACTG	1560
GAACTGATTG	TGCTAAGCAA	GCTATGGATT	TCATACATGA	AATCGGTTGG	CTTCTTCACA	1620
GAAGTAAACT	TGGGAATCA	GACCCAAATC	CAGGCGTTTT	CCCATTAAATA	CGCTTCCAGT	1680
GGCTAATCGA	GTTCTCAATG	GATCGAGAGT	GGTGGCGTGT	GATCAGAAAG	CTATTAAACA	1740
TGTTCTTTGA	TGGAGCTGTT	GGTGAATTTT	CTTCTCTCTC	TAATGCCACA	CTGTCAGAAC	1800
TGTGCCTTCT	TCACAGAGCC	GTGAGGAAAA	ACTCTAAGCC	TATGGTTGAA	ATGCTCTTGA	1860
GATATATTCC	CAAGCAACAG	AGAAACAGCT	TGTTTAGACC	CGATGCTGCT	GGTCCAGCCG	1920
GCTTAACACC	TCTTCATATT	GCAGCTGGTA	AAGACGGTTC	AGAAGATGTG	TTGGATGCGC	1980
TAACAGAAGA	TCCTGCAATG	GTGGGGATTG	AAGCGTGGAA	GACATGTGGA	GACAGCACAG	2040
GCTTCACACC	AGAAGACTAC	GCACGCTTAC	GCGGTCACCT	CTCATAATC	CACTTGATTG	2100
AACGCAAGAT	CAATAAAAAG	TCAACAACCTG	AAGATCATGT	TGTGGTCAAC	ATCCCAGTTT	2160
CTTTCTCAGA	CAGAGAGCAG	AAAGAACCAA	AATCAGGTCC	GATGGCTTCA	GCCTTGGAGA	2220
TCACACAGAT	TCCATGCAAG	CTCTGTGACC	ATAAACTGGT	GTATGGGACA	ACACGCAGGT	2280
CTGTAGCGTA	CAGACCAGCT	ATGTTGTCAA	TGGTGGCGAT	TGCTGCGGTT	TGCGTCTGTG	2340
TGGCACTTCT	GTTTAAGAGT	TGCCCGGAAG	TGCTCTATGT	GTTTCAACCG	TTCAGGTGGG	2400
AGTTATTGGA	CTATGGAACA	AGCTGAGTGT	AAGTCTACTT	TGAAAGATCT	TCTAAGATAT	2460
ATATATGAAT	GTTACTTATA	TAAAACCATA	GAGGTGTGAT	TTCTATATGT	AACTATATGA	2520
GTATAAGATA	TAGAGACATG	TTGGAGAAGA	AGATTGTTGT	TATTATTGTT	GTTGTTGTTG	2580
TTGTGTAAAA	GCCTCTCCTA	TCTCTCTCGA	ACCTAAGGAT	TCTCTCTCTG	ATTAGTATAT	2640
TTTTTGTTTG	ACAAAAAAA	AAAAAAA	AAAAAAA	AA		2682

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 3A52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

Met Glu Ala Arg Ile Asp Glu Gly Gly Glu Ala Gln Gln Phe Tyr Gly
 1             5             10             15

Ser Val Gly Asn Ser Ser Asn Ser Ser Ser Ser Cys Ser Asp Glu Gly
          20             25             30

Asn Asp Lys Lys Arg Arg Ala Val Ala Ile Gln Gly Asp Thr Asn Gly
          35             40             45

Ala Leu Thr Leu Asn Leu Asn Gly Glu Ser Asp Gly Leu Phe Pro Ala
          50             55             60

Lys Lys Thr Lys Ser Gly Ala Val Cys Gln Val Glu Asn Cys Glu Ala
          65             70             75             80

Asp Leu Ser Lys Val Lys Asp Tyr His Arg Arg His Lys Val Cys Glu
          85             90             95

Met His Ser Lys Ala Thr Ser Ala Thr Val Gly Gly Ile Leu Gln Arg
          100            105            110

Phe Cys Gln Gln Cys Ser Arg Phe His Leu Leu Pro Gly Phe Asp Asp
          115            120            125

Gly Lys Arg Ser Cys Arg Arg Arg Leu Ala Gly His Asn Lys Arg Pro
          130            135            140

```

Arg	Lys	Thr	Asn	Pro	Glu	Pro	Gly	Ala	Asn	Gly	Asn	Pro	Ser	Asp	Asp	145	150	155	160
His	Ser	Ser	Asn	Tyr	Leu	Leu	Ile	Thr	Leu	Leu	Lys	Ile	Leu	Ser	Asn	165	170	175	
Met	His	Asn	His	Thr	Gly	Asp	Gln	Asp	Leu	Met	Ser	His	Leu	Leu	Lys	180	185	190	
Ser	Leu	Val	Ser	His	Ala	Gly	Glu	Gln	Leu	Gly	Lys	Asn	Leu	Val	Glu	195	200	205	
Leu	Leu	Leu	Gln	Gly	Arg	Arg	Ser	Gln	Gly	Ser	Leu	Asn	Ile	Gly	Asn	210	215	220	
Ser	Ala	Leu	Leu	Gly	Ile	Glu	Gln	Ala	Pro	Gln	Glu	Glu	Leu	Lys	Gln	225	230	235	240
Phe	Ser	Ala	Arg	Gln	Asp	Gly	Thr	Ala	Thr	Glu	Asn	Arg	Ser	Glu	Lys	245	250	255	
Gln	Val	Lys	Met	Asn	Asp	Phe	Asp	Leu	Asn	Asp	Ile	Tyr	Ile	Asp	Ser	260	265	270	
Asp	Asp	Thr	Asp	Val	Glu	Arg	Ser	Pro	Pro	Pro	Thr	Asn	Pro	Ala	Thr	275	280	285	
Ser	Ser	Leu	Asp	Tyr	Pro	Ser	Trp	Ile	His	Gln	Ser	Ser	Pro	Pro	Gln	290	295	300	
Thr	Ser	Arg	Asn	Ser	Asp	Ser	Ala	Ser	Asp	Gln	Ser	Pro	Ser	Ser	Ser	305	310	315	320
Ser	Glu	Asp	Ala	Gln	Met	Arg	Thr	Gly	Arg	Ile	Val	Phe	Lys	Leu	Phe	325	330	335	
Gly	Lys	Glu	Pro	Asn	Glu	Phe	Pro	Ile	Val	Leu	Arg	Gly	Gln	Ile	Leu	340	345	350	
Asp	Trp	Leu	Ser	His	Ser	Pro	Thr	Asp	Met	Glu	Ser	Tyr	Ile	Arg	Pro	355	360	365	
Gly	Cys	Ile	Val	Leu	Thr	Ile	Tyr	Leu	Arg	Gln	Ala	Glu	Thr	Ala	Trp	370	375	380	
Glu	Glu	Leu	Ser	Asp	Asp	Leu	Gly	Phe	Ser	Leu	Gly	Lys	Leu	Leu	Asp	385	390	395	400

Leu Ser Asp Asp Pro Leu Trp Thr Thr Gly Trp Ile Tyr Val Arg Val
 405 410 415
 Gln Asn Gln Leu Ala Phe Val Tyr Asn Gly Gln Val Val Val Asp Thr
 420 425 430
 Ser Leu Ser Leu Lys Ser Arg Asp Tyr Ser His Ile Ile Ser Val Lys
 435 440 445
 Pro Leu Ala Ile Ala Ala Thr Glu Lys Ala Gln Phe Thr Val Lys Gly
 450 455 460
 Met Asn Leu Arg Arg Arg Gly Thr Arg Leu Leu Cys Ser Val Glu Gly
 465 470 475 480
 Lys Tyr Leu Ile Gln Glu Thr Thr His Asp Ser Thr Thr Arg Glu Asp
 485 490 495
 Asp Asp Phe Lys Asp Asn Ser Glu Ile Val Glu Cys Val Asn Phe Ser
 500 505 510
 Cys Asp Met Pro Ile Leu Ser Gly Arg Gly Phe Met Glu Ile Glu Asp
 515 520 525
 Gln Gly Leu Ser Ser Ser Phe Phe Pro Phe Leu Val Val Glu Asp Asp
 530 535 540
 Asp Val Cys Ser Glu Ile Arg Ile Leu Glu Thr Thr Leu Glu Phe Thr
 545 550 555 560
 Gly Thr Asp Ser Ala Lys Gln Ala Met Asp Phe Ile His Glu Ile Gly
 565 570 575
 Trp Leu Leu His Arg Ser Lys Leu Gly Glu Ser Asp Pro Asn Pro Gly
 580 585 590
 Val Phe Pro Leu Ile Arg Phe Gln Trp Leu Ile Glu Phe Ser Met Asp
 595 600 605
 Arg Glu Trp Cys Ala Val Ile Arg Lys Leu Leu Asn Met Phe Phe Asp
 610 615 620
 Gly Ala Val Gly Glu Phe Ser Ser Ser Ser Asn Ala Thr Leu Ser Glu
 625 630 635 640
 Leu Cys Leu Leu His Arg Ala Val Arg Lys Asn Ser Lys Pro Met Val
 645 650 655
 Glu Met Leu Leu Arg Tyr Ile Pro Lys Gln Gln Arg Asn Ser Leu Phe

660	665	670
Arg Pro Asp Ala Ala Gly Pro Ala Gly Leu Thr Pro Leu His Ile Ala		
675	680	685
Ala Gly Lys Asp Gly Ser Glu Asp Val Leu Asp Ala Leu Thr Glu Asp		
690	695	700
Pro Ala Met Val Gly Ile Glu Ala Trp Lys Thr Cys Arg Asp Ser Thr		
705	710	715
Gly Phe Thr Pro Glu Asp Tyr Ala Arg Leu Arg Gly His Phe Ser Tyr		
725	730	735
Ile His Leu Ile Gln Arg Lys Ile Asn Lys Lys Ser Thr Thr Glu Asp		
740	745	750
His Val Val Val Asn Ile Pro Val Ser Phe Ser Asp Arg Glu Gln Lys		
755	760	765
Glu Pro Lys Ser Gly Pro Met Ala Ser Ala Leu Glu Ile Thr Gln Ile		
770	775	780
Pro Cys Lys Leu Cys Asp His Lys Leu Val Tyr Gly Thr Thr Arg Arg		
785	790	795
Ser Val Ala Tyr Arg Pro Ala Met Leu Ser Met Val Ala Ile Ala Ala		
805	810	815
Val Cys Val Cys Val Ala Leu Leu Phe Lys Ser Cys Pro Glu Val Leu		
820	825	830
Tyr Val Phe Gln Pro Phe Arg Trp Glu Leu Leu Asp Tyr Gly Thr Ser		
835	840	845

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: 4B11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CAGCGGAAGA GCTCACCGTT GAAGAGAGGA ATCTCCTCTC TGTTGCTTAC AAAAACGTGA	60
TCGGATCTCT ACGCGCCGCC TGGAGGATCG TGTCTTCGAT TGAGCAGAAG GAAGAGAGTA	120
GGAAGAACGA CGAGCACGTG TCGCTTGTC AAGGATTACAG ATCTAAAGTT GAGTCTGAGC	180
TTTCTTCTGT TTGCTCTGGA ATCCTTAAGC TCCTTGACTC GCATCTGATC CCATCTGCTG	240
GAGCGAGTGA GTCTAAGGTC TTTTACTTGA AGATGAAAGG TGATTATCAT CGGTACATGG	300
CTGAGTTTAA GTCTGGTGAT GAGAGGAAAA CTGCTGCTGA AGATACCATG CTCGCTTACA	360
AAGCAGCTCA GGATATCGCA GCTGCGGATA TGGCACCTAC TCATCCGATA AGGCTTGCTC	420
TGGCCCTGAA TTTCTCAGTG TTCTACTATG AGATTCTCAA TTCTTCAGAC AAAGCTTGTA	480
ACATGGCCAA ACAGGCTTTT GAGGAAGCCA TAGCTGAGCT TGACACTCTG GGAGAAGAAT	540
CCTACAAAGA CAGCACTCTC ATAATGCAGT TGCTGA	576

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: 4B11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Ala	Ala	Thr	Leu	Gly	Arg	Asp	Gln	Tyr	Val	Tyr	Met	Ala	Lys	Leu	1	5	10	15
Ala	Glu	Gln	Ala	Glu	Arg	Tyr	Glu	Glu	Met	Val	Gln	Phe	Met	Glu	Gln	20	25	30	
Leu	Val	Thr	Gly	Ala	Thr	Pro	Ala	Glu	Glu	Leu	Thr	Val	Glu	Glu	Arg	35	40	45	
Asn	Leu	Leu	Ser	Val	Ala	Tyr	Lys	Asn	Val	Ile	Gly	Ser	Leu	Arg	Ala	50	55	60	
Ala	Trp	Arg	Ile	Val	Ser	Ser	Ile	Glu	Gln	Lys	Glu	Glu	Ser	Arg	Lys	65	70	75	80
Asn	Asp	Glu	His	Val	Ser	Leu	Val	Lys	Asp	Tyr	Arg	Ser	Lys	Val	Glu	85	90	95	
Ser	Glu	Leu	Ser	Ser	Val	Cys	Ser	Gly	Ile	Leu	Lys	Leu	Leu	Asp	Ser	100	105	110	
His	Leu	Ile	Pro	Ser	Ala	Gly	Ala	Ser	Glu	Ser	Lys	Val	Phe	Tyr	Leu	115	120	125	
Lys	Met	Lys	Gly	Asp	Tyr	His	Arg	Tyr	Met	Ala	Glu	Phe	Lys	Ser	Gly	130	135	140	
Asp	Glu	Arg	Lys	Thr	Ala	Ala	Glu	Asp	Thr	Met	Leu	Ala	Tyr	Lys	Ala	145	150	155	160
Ala	Gln	Asp	Ile	Ala	Ala	Ala	Asp	Met	Ala	Pro	Thr	His	Pro	Ile	Arg	165	170	175	
Leu	Gly	Leu	Ala	Leu	Asn	Phe	Ser	Val	Phe	Tyr	Tyr	Glu	Ile	Leu	Asn	180	185	190	
Ser	Ser	Asp	Lys	Ala	Cys	Asn	Met	Ala	Lys	Gln	Ala	Phe	Glu	Glu	Ala	195	200	205	
Ile	Ala	Glu	Leu	Asp	Thr	Leu	Gly	Glu	Glu	Ser	Tyr	Lys	Asp	Ser	Thr	210	215	220	
Leu	Ile	Met	Gln	Leu	Leu	Arg	Asp	Asn	Leu	Thr	Leu	Trp	Thr	Ser	Asp	225	230	235	240

Met Gln Glu Gln Met Asp Glu Ala
245

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 4A24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CGCCGCCACC GCGATGTACG TGATCTACCA CCCTCGTCCG CCGTCGTTCT CCGTCCCGTC	60
AATAAGAATC AGCCGCGTGA ACCTAACAAC CTCCTCTGAT TCCTCCGTCT CTCATCTCTC	120
TTCCITCTTC AACTTCACTC TAATCTCAGA GAATCCAAAC CAACACCTCT CTTTCTCTTA	180
CGATCCTTTC ACGTCCACCG TTAATTCAGC TAAATCCGGT ACGATGCTCG GTAACGGAAC	240
TGTTCCTGCT TTCTTCAGCG ATAACGGTAA CAAACTTCG TTTCACGGCG TGATCGCTAC	300
GTCTACAGCG GCGCGTGAGT TAGATCCGGA TGAAGCTAAG CATCTGAGAT CAGATCTGAC	360
GCGCGCGCGT GTAGGATATG AGATCGAGAT GAGAACTAAA GTGAAGATGA TAATGGGGAA	420
GCTGAAGAGT GAAGGAGTAG AGATCAAAGT GACATGTTGA AGGATTTGAA GGAACATATC	480
CAAAAGGTAA AACTCCAATT GTAGCTACTT CTAAAAAAC TAAGTGTAAG TCTGATCTTA	540
GTGTCAAGTC TGGAAATGGA TTTCTAAAGG AATTGATAA TTTCACATTG AAATTCTATA	600
TATCTCTCTT TTCTCTGGA TTTGTGAAAC TTTGGATGAT CAAAGAATTC TTCATTGTC	659

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 4A24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Arg	Ile	Cys	Cys	Cys	Cys	Phe	Trp	Ser	Ile	Leu	Ile	Ile	Leu	Ile	Leu	1	5	10	15
Ala	Leu	Met	Thr	Ala	Ile	Ala	Ala	Thr	Ala	Met	Tyr	Val	Ile	Tyr	His	20	25	30	
Pro	Arg	Pro	Pro	Ser	Phe	Ser	Val	Pro	Ser	Ile	Arg	Ile	Ser	Arg	Val	35	40	45	
Asn	Leu	Thr	Thr	Ser	Ser	Asp	Ser	Ser	Val	Ser	His	Leu	Ser	Ser	Phe	50	55	60	
Phe	Asn	Phe	Thr	Leu	Ile	Ser	Glu	Asn	Pro	Asn	Gln	His	Leu	Ser	Phe	65	70	75	80
Ser	Tyr	Asp	Pro	Phe	Thr	Val	Thr	Val	Asn	Ser	Ala	Lys	Ser	Gly	Thr	85	90	95	
Met	Leu	Gly	Asn	Gly	Thr	Val	Pro	Ala	Phe	Phe	Ser	Asp	Asn	Gly	Asn	100	105	110	
Lys	Thr	Ser	Phe	His	Gly	Val	Ile	Ala	Thr	Ser	Thr	Ala	Ala	Arg	Glu	115	120	125	
Leu	Asp	Pro	Asp	Glu	Ala	Lys	His	Leu	Arg	Ser	Asp	Leu	Thr	Arg	Ala	130	135	140	

Arg Val Gly Tyr Glu Ile Glu Met Arg Thr Lys Val Lys Met Ile Met
 145 150 155 160

Gly Lys Leu Lys Ser Glu Gly Val Glu Ile Lys Val Thr Cys
 165 170

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 3B76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCTCCTCACTC CAGGCCAGCC AACAAAAGAA CCTACATTTA TTCCAGTGGT TGTTGGTCTT	60
TTGGACTCAA GTGGGAAAGA CATTACTCTT TCCTCTGTTC ATTATGATGG TACAGTGCAG	120
ACCATTTTCAG GCAGCAGCAC AATACTTCGA GTGACAAGAA ACAAGAAGAG TTTGTGTTTT	180
CTGATATACC AGAAAGACCT GTTCCGTCCC TATTTAGGGG ATTACAGCCCC AGTTCGTGTT	240
GAAACTGATC TCTCTAATGA TGAATTATTC TTCCTCCTAG CACATGATTC AGATGAATTC	300
AATAGGTGGG AGGCCGGTCA AGTTCTGGCA AGAAAGCTGA TGCTGAACCTT AGTTTCTGAT	360
TTCCAGCAAA ATAAACCGTT GGCTCTAAAC CAAAATTTG TGCAAGGTCT CGGCAGTGTG	420
CTTTCTGACT CAAGCTTGA CAAGGAATTT ATAGCCAAAG CAATAACACT ACCTGGGGAG	480
GGAGAGATAA TGGACATGAT GGCCGTGGCG GATCCTGATG CTGTTTCATGC TGTTAGAAAG	540
TTTGTACGAA AGCAGCTTGC ATCTGAACCT AAGGAGGAGC TTCT	584

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 283 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Arabidopsis thaliana*
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: 3B76
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
- | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Pro | Pro | Thr | Pro | Gly | Gln | Pro | Thr | Lys | Glu | Pro | Thr | Phe | Ile | Pro | Val | 1 | 5 | 10 | 15 |
| Val | Val | Gly | Leu | Leu | Asp | Ser | Ser | Gly | Lys | Asp | Ile | Thr | Leu | Ser | Ser | 20 | 25 | 30 | |
| Val | His | Tyr | Asp | Gly | Thr | Val | Gln | Thr | Ile | Thr | Gly | Ser | Ser | Thr | Ile | 35 | 40 | 45 | |
| Leu | Arg | Val | Thr | Lys | Lys | Gln | Glu | Glu | Phe | Val | Phe | Ser | Asp | Ile | Pro | 50 | 55 | 60 | |
| Glu | Arg | Pro | Val | Pro | Ser | Leu | Phe | Arg | Gly | Phe | Ser | Ala | Pro | Val | Arg | 65 | 70 | 75 | 80 |
| Val | Glu | Thr | Asp | Leu | Ser | Asn | Asp | Asp | Leu | Phe | Phe | Leu | Leu | Ala | His | 85 | 90 | 95 | |
| Asp | Ser | Asp | Glu | Phe | Asn | Arg | Trp | Glu | Ala | Gly | Gln | Val | Leu | Ala | Arg | 100 | 105 | 110 | |
| Lys | Leu | Met | Leu | Asn | Leu | Val | Ser | Asp | Phe | Gln | Gln | Asn | Lys | Pro | Leu | 115 | 120 | 125 | |
| Ala | Leu | Asn | Pro | Lys | Phe | Val | Gln | Gly | Leu | Gly | Ser | Val | Leu | Ser | Asp | 130 | 135 | 140 | |

Ser	Ser	Leu	Asp	Lys	Glu	Phe	Ile	Ala	Lys	Ala	Ile	Thr	Leu	Pro	Gly
145					150				155						160
Glu	Gly	Glu	Ile	Met	Asp	Met	Met	Ala	Val	Ala	Asp	Pro	Asp	Ala	Val
				165					170					175	
His	Ala	Val	Arg	Lys	Phe	Val	Arg	Lys	Gln	Leu	Ala	Ser	Glu	Leu	Lys
			180					185					190		
Glu	Glu	Leu	Lys	Ile	Val	Glu	Asn	Asn	Arg	Ser	Thr	Glu	Ala	Tyr	Val
		195					200					205			
Phe	Asp	His	Ser	Asn	Met	Ala	Arg	Arg	Ala	Leu	Lys	Asn	Thr	Ala	Leu
	210					215					220				
Ala	Tyr	Leu	Ala	Ser	Leu	Glu	Asp	Pro	Ala	Tyr	Met	Gly	Thr	Cys	Thr
225					230					235					240
Glu	Arg	Ile	Gln	Gly	Gly	His	Gln	Phe	Asp	Arg	Pro	Ile	Cys	Cys	Phe
			245					250					255		
Gly	Thr	Leu	Ser	Gln	Asn	Pro	Gly	Lys	Thr	Arg	Glu	Arg	Thr	Phe	Leu
		260						265					270		
Pro	Asp	Phe	Tyr	Glu	Gln	Val	Ala	Gly	Thr	Ile					
	275						280								

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 4A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ACCAGGAGGG GAAAAAGTCT TACCCCATGG ACATCCCGGG GATTGAGTGT TACCCGAAAA 60
 GGATGAAGAA TGGTATTCTT CCGTCGTGGA CCCCATGCAC CCATTGGGAA AGCCGTGTGG 120
 CGTTTTCTTT CAGGGATGAT AGAAAAGTGC TCCCTTGGGA TGGAAAGGAG GAGCCTTTAC 180
 TGGTAGTGGC CGATAGGGTG AGGAATGTTG TGGAGGCTGA TGACGGGTAT TATCTCGTGG 240
 TGGCTGAGAA CGGACTTAAG CTAGAGAAAG GATCAGATTT GAAGGCGAGA GAGGTGAAGG 300
 AGAGTTTAGG GATGGTTGTT TTGGTGGTGA GGCCGCCAAG AGAAGATGAT GATGATTGGC 360
 AGACAAGTCA TCAGAACTGG GACTGAATTA ATAGAATCAA TACTCATATG CTGTAACTGA 420
 TTACGGAGTC ATCATGGTCA TGTAATAATT TTGGATAAAG GTGGTAACTT TTTGTTCTAA 480
 GATACAATCA GAAACAGAGC AATATTTTTT TCTAAAAAAA AAAAAAAAAA AAAA 534

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 4A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Asp Ile Pro Gly Ile Glu Cys Tyr Pro Lys Arg Met Lys Asn Gly
 1 5 10 15
 Ile Pro Pro Ser Trp Thr Pro Cys Thr His Trp Glu Ser Arg Val Ala
 20 25 30

Phe Ser Phe Arg Asp Asp Arg Lys Val Leu Pro Trp Asp Gly Lys Glu
 35 40 45
 Glu Pro Leu Leu Val Val Ala Asp Arg Val Arg Asn Val Val Glu Ala
 50 55 60
 Asp Asp Gly Tyr Tyr Leu Val Val Ala Glu Asn Gly Leu Lys Leu Glu
 65 70 75 80
 Lys Gly Ser Asp Leu Lys Ala Arg Glu Val Lys Glu Ser Leu Gly Met
 85 90 95
 Val Val Leu Val Val Arg Pro Pro Arg Glu Asp Asp Asp Asp Trp Gln
 100 105 110
 Thr Ser His Gln Asn Trp Asp
 115

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: primer V6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATGCTTTGCA TAACTTTGAG G

21

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: primer T7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AATACGACTC ACTATAG

17

18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186
2187
2188
2189
2190
2191
2192
21